

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:24:58 ; Search time 172.793 Seconds
(without alignments)
809.667 Million cell updates/sec

Title: US-10-053-975A-1
Perfect score: 2047
Sequence: 1 MAVSESQLKKMVSKYKYRDL.....FQLRALMQKARKTAGLSDLY 390

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2047	100.0	390	2	AAW93424	Aaw93424 Human NHT
2	2047	100.0	390	5	ABP52191	Abp52191 Human tum
3	2047	100.0	390	6	ABG73787	Abg73787 Human tum
4	2047	100.0	390	7	ADC35176	Adc35176 Novel hum
5	2047	100.0	390	8	ADF91425	Adf91425 TSG101 #S
6	2047	100.0	390	8	ADL82957	Adl82957 Human PRO
7	2047	100.0	390	8	ADN12256	Adn12256 Human TSG
8	2047	100.0	390	8	ADO43235	Ado43235 Human TSG
9	2047	100.0	390	8	ADO43233	Ado43233 Human TSG

10	2047	100.0	390	8	ADP82614	Adp82614	Human	tum
11	2042	99.8	390	6	AAE34885	Aae34885	Human	Tsg
12	2002	97.8	380	2	AAW19111	Aaw19111	Human	tum
13	1945.5	95.0	391	6	AAE34884	Aae34884	Mouse	Tsg
14	1945.5	95.0	391	7	ADB85228	Adb85228	Mouse	tum
15	1900.5	92.8	381	2	AAW19110	Aaw19110	Mouse	tum
16	1900.5	92.8	381	2	AAW93425	Aaw93425	Mouse	tsg
17	1900.5	92.8	381	6	ABG73788	Abg73788	Murine	ts
18	1900.5	92.8	381	7	ADC35178	Adc35178	Human	tsg
19	1404	68.6	307	5	ABP41729	Abp41729	Human	ova
20	1162	56.8	237	4	AAE09328	Aae09328	Human	int
21	809.5	39.5	331	4	ABB64607	Abb64607	Drosophil	
22	776	37.9	145	8	ADF91424	Adf91424	TSG101UEV	
23	479	23.4	90	3	AAG01689	Aag01689	Human	sec
24	455	22.2	398	3	AAG06370	Aag06370	Arabidops	
25	455	22.2	398	8	ADN73283	Adn73283	Thale	cre
26	455	22.2	412	3	AAG06369	Aag06369	Arabidops	
27	435	21.3	379	5	ABP43551	Abp43551	L-lactate	
28	435	21.3	379	8	ADH13697	Adh13697	Human	ENZ
29	424	20.7	340	3	AAG06371	Aag06371	Arabidops	
30	390	19.1	87	8	ABO55273	Abo55273	Human	gen
31	380	18.6	322	3	AAG13898	Aag13898	Arabidops	
32	371	18.1	341	4	AAB93473	Aab93473	Human	pro
33	371	18.1	433	7	ADM29340	Adm29340	Human	nov
34	346	16.9	146	3	AAB53717	Aab53717	Human	col
35	339	16.6	452	4	AAU23116	Aau23116	Novel	hum
36	328	16.0	73	8	ABO55495	Abo55495	Human	gen
37	267.5	13.1	288	3	AAG13899	Aag13899	Arabidops	
38	161.5	7.9	168	3	AAG13900	Aag13900	Arabidops	
39	161	7.9	485	3	AAB57086	Aab57086	Human	pro
40	160	7.8	466	6	ABO07215	Abo07215	Human	p53
41	160	7.8	466	7	ADD47589	Add47589	Human	Pro
42	160	7.8	466	7	ADI15879	Adi15879	Human	PP
43	160	7.8	466	7	ADJ68571	Adj68571	Human	hea
44	153	7.5	218	4	ABG18833	Abg18833	Novel	hum
45	151	7.4	466	2	AAR07084	Aar07084	Recombina	

ALIGNMENTS

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:40:45 ; Search time 35.897 Seconds
(without alignments)
1045.338 Million cell updates/sec

Title: US-10-053-975A-1
Perfect score: 2047
Sequence: 1 MAVSESQLKKMVSKYKYRDL.....FQLRALMQKARKTAGLSDLY 390

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	658	32.1	404	2	H88650	protein C09G12.9 [
2	388	19.0	83	2	I48283	gene CC2 protein -	
3	153.5	7.5	169	2	T34520	hypothetical prote	
4	148.5	7.3	397	2	JC8036	hepatocellular car	
5	147	7.2	488	1	LUHU7	annexin VII, long	
6	145.5	7.1	212	2	S74288	hypothetical prote	
7	142	6.9	505	2	A53152	annexin XI - human	
8	141	6.9	463	2	S29170	annexin VII - mous	
9	138.5	6.8	827	2	T39608	zinc finger transc	
10	136.5	6.7	503	1	LURB11	annexin XI - rabbi	
11	135.5	6.6	437	2	T14192	extensin homolog T	
12	134	6.5	198	2	D70509	hypothetical prote	
13	134	6.5	485	2	T37550	hypothetical coile	

14	132.5	6.5	671	2	T36037	probable export as
15	131.5	6.4	370	2	T42532	hypothetical prote
16	131	6.4	1613	2	S39059	protein BRG1 - hum
17	131	6.4	1880	2	T18531	tractin - medicina
18	130.5	6.4	338	2	I53043	transforming prote
19	130	6.4	1647	2	S45252	SNF2beta protein -
20	128.5	6.3	1006	2	T42731	atrophin-1 related
21	128	6.3	139	2	H84809	hypothetical prote
22	128	6.3	3942	2	T42730	Bassoon protein -
23	127	6.2	1184	2	G01763	atrophin-1 - human
24	126.5	6.2	678	2	H88187	protein C18H9.8 [i
25	126	6.2	1453	2	S21626	collagen alpha 1(I
26	125	6.1	2715	2	T13049	eyelid - fruit fly
27	124.5	6.1	669	2	T28754	hypothetical prote
28	124.5	6.1	990	2	T14756	hypothetical prote
29	124	6.1	964	2	T21865	hypothetical prote
30	123.5	6.0	279	2	T05421	hypothetical prote
31	123.5	6.0	380	2	S51797	vasodilator-stimul
32	123	6.0	564	2	H70804	hypothetical prote
33	122	6.0	887	1	S57219	1-phosphatidylinos
34	122	6.0	978	2	A70387	conserved hypothet
35	122	6.0	1181	2	C86349	F8K7.4 protein - A
36	121.5	5.9	551	2	S57447	HPBR11-7 protein -
37	121	5.9	792	2	T49989	hypothetical prote
38	120.5	5.9	1902	2	C97702	cell surface antig
39	119.5	5.8	503	1	LUBO11	annexin XI form A
40	119.5	5.8	505	1	S23447	annexin XI form B
41	119	5.8	577	2	T09024	proline-rich prote
42	119	5.8	859	2	H70327	DNA mismatch repai
43	119	5.8	1357	2	T29265	hypothetical prote
44	119	5.8	1422	2	T24212	hypothetical prote
45	118.5	5.8	384	2	S51796	vasodilator-stimul

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:26:03 ; Search time 188.612 Seconds
 (without alignments)
 1189.726 Million cell updates/sec

Title: US-10-053-975A-1
 Perfect score: 2047
 Sequence: 1 MAVSESQLKKMVSKYKYRDL.....FQLRALMQKARKTAGLSLDLY 390

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_02:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2047	100.0	390	1 T101_HUMAN	Q99816 homo sapien
2	2041	99.7	390	2 Q9BUM5	Q9bum5 homo sapien
3	1945.5	95.0	391	1 T101_MOUSE	Q61187 mus musculu
4	1927.5	94.2	391	2 Q6IRE4	Q6ire4 rattus norv
5	1927.5	94.2	391	2 AAH70951	Aah70951 rattus no
6	1908.5	93.2	391	2 Q7TSE5	Q7tse5 rattus norv
7	1899	92.8	392	2 Q9I8G8	Q9i8g8 chelonia my
8	1705.5	83.3	390	2 Q6IQ70	Q6iq70 brachydanio
9	1705.5	83.3	390	2 AAH71540	Aah71540 brachydan
10	1685	82.3	394	2 Q6NUD5	Q6nud5 xenopus lae
11	1685	82.3	394	2 AAH68660	Aah68660 xenopus l
12	1682.5	82.2	395	2 Q6P2Z8	Q6p2z8 xenopus tro
13	1682.5	82.2	395	2 AAH64236	Aah64236 xenopus t
14	1024.5	50.0	408	2 Q9VVA7	Q9vva7 drosophila
15	976	47.7	402	2 Q7Q6B6	Q7q6b6 anopheles g

16	754.5	36.9	425	2	O76258	O76258	caenorhabdi
17	749.5	36.6	326	2	Q6DDX9	Q6ddx9	xenopus lae
18	599	29.3	249	2	Q8MQZ0	Q8mqz0	drosophila
19	522	25.5	114	2	Q7T2M2	Q7t2m2	ameiurus ne
20	455	22.2	398	2	Q9LHG8	Q9lhg8	arabidopsis
21	435	21.3	379	2	Q8IX04	Q8ix04	homo sapien
22	432	21.1	580	2	Q7S4R9	Q7s4r9	neurospora
23	429.5	21.0	249	2	Q7TQD3	Q7tqd3	mus musculu
24	427	20.9	174	2	O08761	O08761	mus musculu
25	398	19.4	471	2	Q6DBY5	Q6dby5	brachydanio
26	396.5	19.4	402	2	Q6ESB7	Q6esb7	oryza sativ
27	391	19.1	368	2	Q9FFY6	Q9fffy6	arabidopsis
28	388	19.0	83	2	Q6LBE4	Q6lbe4	mus musculu
29	388	19.0	83	2	CAA57762	Caa57762	mus muscu
30	371	18.1	177	2	Q96FF5	Q96ff5	homo sapien
31	371	18.1	341	2	Q9NUX7	Q9nux7	homo sapien
32	341	16.7	357	2	Q6P2F0	Q6p2f0	homo sapien
33	341	16.7	357	2	AAH64566	Aah64566	homo sapi
34	303	14.8	385	1	ST22_YEAST	P25604	saccharomyc
35	301.5	14.7	378	2	Q873M7	Q873m7	yarrowia li
36	301.5	14.7	378	2	Q6C148	Q6c148	yarrowia li
37	294	14.4	111	2	Q8BU96	Q8bu96	mus musculu
38	294	14.4	468	2	Q6FS29	Q6fs29	candida gla
39	239	11.7	496	2	Q6BID5	Q6bid5	debaryomyce
40	215	10.5	445	2	Q75EU1	Q75eu1	ashbya goss
41	215	10.5	445	2	AAS50360	Aas50360	ashbya go
42	169	8.3	376	2	P78998	P78998	saccharomyc
43	160	7.8	466	1	ANX7_HUMAN	P20073	homo sapien
44	160	7.8	466	2	BAB93492	Bab93492	homo sapi
45	160	7.8	466	2	AAP35851	Aap35851	homo sapi

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:24:58 ; Search time 62.0281 Seconds
 (without alignments)
 809.667 Million cell updates/sec

Title: US-10-053-975A-1_COPY_1_140
 Perfect score: 750
 Sequence: 1 MAVSESQLKKMVSKYKYRDL.....QSDLLGLIQVMIVVFGDEPP 140

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	750	100.0	145	8	ADF91424	Adf91424 TSG101UEV
2	750	100.0	237	4	AAE09328	Aae09328 Human int
3	750	100.0	390	2	AAW93424	Aaw93424 Human NHT
4	750	100.0	390	5	ABP52191	Abp52191 Human tum
5	750	100.0	390	6	AAE34885	Aae34885 Human Tsg
6	750	100.0	390	6	ABG73787	Abg73787 Human tum
7	750	100.0	390	7	ADC35176	Adc35176 Novel hum
8	750	100.0	390	8	ADF91425	Adf91425 TSG101 #S
9	750	100.0	390	8	ADL82957	Adl82957 Human PRO

10	750	100.0	390	8	ADN12256	Adn12256	Human	TSG
11	750	100.0	390	8	ADO43235	Ado43235	Human	TSG
12	750	100.0	390	8	ADO43233	Ado43233	Human	TSG
13	750	100.0	390	8	ADP82614	Adp82614	Human	tum
14	705	94.0	380	2	AAW19111	Aaw19111	Human	tum
15	693	92.4	391	6	AAE34884	Aae34884	Mouse	Tsg
16	693	92.4	391	7	ADB85228	Adb85228	Mouse	tum
17	648	86.4	381	2	AAW19110	Aaw19110	Mouse	tum
18	648	86.4	381	2	AAW93425	Aaw93425	Mouse	tsg
19	648	86.4	381	6	ABG73788	Abg73788	Murine	ts
20	648	86.4	381	7	ADC35178	Adc35178	Human	tsg
21	479	63.9	90	3	AAG01689	Aag01689	Human	sec
22	427	56.9	379	5	ABP43551	Abp43551	L-lactate	
23	427	56.9	379	8	ADH13697	Adh13697	Human	ENZ
24	363	48.4	341	4	AAB93473	Aab93473	Human	pro
25	363	48.4	433	7	ADM29340	Adm29340	Human	nov
26	346	46.1	146	3	AAB53717	Aab53717	Human	col
27	331	44.1	452	4	AAU23116	Aau23116	Novel	hum
28	328	43.7	73	8	ABO55495	Abo55495	Human	gen
29	276.5	36.9	398	3	AAG06370	Aag06370	Arabidops	
30	276.5	36.9	398	8	ADN73283	Adn73283	Thale	cre
31	276.5	36.9	412	3	AAG06369	Aag06369	Arabidops	
32	245.5	32.7	340	3	AAG06371	Aag06371	Arabidops	
33	239	31.9	331	4	ABB64607	Abb64607	Drosophil	
34	201.5	26.9	322	3	AAG13898	Aag13898	Arabidops	
35	107	14.3	307	5	ABP41729	Abp41729	Human	ova
36	106	14.1	123	4	ABG03740	Abg03740	Novel	hum
37	89.5	11.9	527	4	AAM80181	Aam80181	Human	pro
38	89.5	11.9	1648	3	AAB43174	Aab43174	Human	ORF
39	89.5	11.9	1867	4	AAB95564	Aab95564	Human	pro
40	89.5	11.9	4829	4	AAB97833	Aab97833	Human	apo
41	89	11.9	288	3	AAG13899	Aag13899	Arabidops	
42	88	11.7	18	8	ADN12257	Adn12257	Human	TSG
43	85.5	11.4	192	3	AAG04759	Aag04759	Arabidops	
44	85.5	11.4	254	7	ADH88640	Adh88640	Enterococ	
45	85.5	11.4	258	7	ADC94862	Adc94862	E. faeciu	

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:40:45 ; Search time 12.8861 Seconds
 (without alignments)
 1045.338 Million cell updates/sec

Title: US-10-053-975A-1_COPY_1_140
 Perfect score: 750
 Sequence: 1 MAVSESQLKKMVSKYKYRDL.....QSDLLGLIQVMIVVFGDEPP 140

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_79:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	299.5	39.9	404	2	H88650	protein C09G12.9 [
2	96.5	12.9	179	2	T34367	hypothetical prote
3	95.5	12.7	212	2	S74288	hypothetical prote
4	87.5	11.7	4845	2	T31067	BIR repeat contain
5	83.5	11.1	666	2	T40172	Glucose inhibited
6	82.5	11.0	940	2	AD1374	internalin protein
7	80	10.7	423	2	T15350	hypothetical prote
8	80	10.7	940	2	AB1744	internalin protein
9	79.5	10.6	800	2	T26683	hypothetical prote
10	79	10.5	1088	1	P1XRPR	inner layer protei
11	78.5	10.5	194	2	S57619	ubiquitin conjugat
12	78.5	10.5	1088	1	P1XRSR	inner layer protei
13	78.5	10.5	1088	2	S13558	VP1 protein - bovi

14	77	10.3	1088	2	S39261	VP1 protein - porc
15	76.5	10.2	144	2	G90107	ubiquitin-conjugat
16	76.5	10.2	458	2	T13819	NADH2 dehydrogenas
17	76	10.1	666	2	D42510	O1L protein - vacc
18	76	10.1	763	2	D83905	hypothetical prote
19	75.5	10.1	708	2	T47650	ABC transporter-li
20	74.5	9.9	147	2	D90126	ubiquitin-conjugat
21	74.5	9.9	754	2	AG1265	protein-export mem
22	74.5	9.9	1088	1	P1XRBR	inner layer protei
23	73.5	9.8	247	2	JU0393	karasurin - Mongol
24	73.5	9.8	247	2	JC5032	karasurin-B - Tric
25	73.5	9.8	289	1	RLTZT	rRNA N-glycosidase
26	73.5	9.8	289	2	JC5606	karasurin C - Tric
27	73.5	9.8	1738	2	S20614	conserved hypothet
28	73	9.7	296	2	F91145	probable methyltra
29	73	9.7	296	2	B85991	probable methyltra
30	73	9.7	296	2	H65118	hypothetical adeni
31	72.5	9.7	154	2	JC6163	ubiquitin-conjugat
32	72.5	9.7	269	2	F85063	hypothetical prote
33	72.5	9.7	803	2	S76106	hypothetical prote
34	72	9.6	218	2	B53516	ubiquitin-protein
35	72	9.6	475	1	S46941	translation initia
36	71.5	9.5	295	2	AC2357	DNA-methyltransfer
37	71.5	9.5	626	2	T08926	hypothetical prote
38	71	9.5	778	2	B71164	probable beta-gala
39	70.5	9.4	240	1	C69114	conserved hypothet
40	70.5	9.4	566	2	A59285	myosin-VIIa motor
41	70	9.3	702	2	S59428	probable membrane
42	70	9.3	888	1	GNLJHD	pol polyprotein -
43	69.5	9.3	154	2	T13578	ubiquitin-conjugat
44	69.5	9.3	230	2	T16479	hypothetical prote
45	69.5	9.3	238	2	AH0164	arginine transport

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:26:03 ; Search time 67.7067 Seconds
(without alignments)
1189.726 Million cell updates/sec

Title: US-10-053-975A-1_COPY_1_140
Perfect score: 750
Sequence: 1 MAVSESQLKKMVSKYKYRDL.....QSDLLGLIQVMIVVFGDEPP 140

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	750	100.0	390	1 T101_HUMAN	Q99816 homo sapien
2	750	100.0	390	2 Q9BUM5	Q9bum5 homo sapien
3	693	92.4	391	1 T101_MOUSE	Q61187 mus musculu
4	693	92.4	391	2 Q6IRE4	Q6ire4 rattus norv
5	693	92.4	391	2 AAH70951	Aah70951 rattus no
6	693	92.4	392	2 Q9I8G8	Q9i8g8 chelonia my
7	684	91.2	391	2 Q7TSE5	Q7tse5 rattus norv
8	676	90.1	326	2 Q6DDX9	Q6ddx9 xenopus lae
9	673	89.7	394	2 Q6NUD5	Q6nud5 xenopus lae
10	673	89.7	394	2 AAH68660	Aah68660 xenopus l
11	670	89.3	395	2 Q6P2Z8	Q6p2z8 xenopus tro
12	670	89.3	395	2 AAH64236	Aah64236 xenopus t
13	650	86.7	390	2 Q6IQ70	Q6iq70 brachydanio
14	650	86.7	390	2 AAH71540	Aah71540 brachydan
15	522	69.6	114	2 Q7T2M2	Q7t2m2 ameiurus ne

16	454	60.5	249	2	Q8MQZ0	Q8mqz0 drosophila
17	454	60.5	408	2	Q9VVA7	Q9vva7 drosophila
18	428	57.1	402	2	Q7Q6B6	Q7q6b6 anopheles g
19	427	56.9	379	2	Q8IX04	Q8ix04 homo sapien
20	415	55.3	174	2	O08761	O08761 mus musculu
21	409.5	54.6	249	2	Q7TQD3	Q7tqd3 mus musculu
22	397	52.9	471	2	Q6DBY5	Q6dby5 brachydanio
23	363	48.4	177	2	Q96FF5	Q96ff5 homo sapien
24	363	48.4	341	2	Q9NUX7	Q9nux7 homo sapien
25	342	45.6	425	2	O76258	O76258 caenorhabdi
26	333	44.4	357	2	Q6P2F0	Q6p2f0 homo sapien
27	333	44.4	357	2	AAH64566	Aah64566 homo sapi
28	280	37.3	111	2	Q8BU96	Q8bu96 mus musculu
29	276.5	36.9	398	2	Q9LHG8	Q9lhg8 arabidopsis
30	252.5	33.7	368	2	Q9FFY6	Q9fffy6 arabidopsis
31	252	33.6	580	2	Q7S4R9	Q7s4r9 neurospora
32	212	28.3	402	2	Q6ESB7	Q6esb7 oryza sativ
33	152.5	20.3	496	2	Q6BID5	Q6bid5 debaryomyce
34	150	20.0	385	1	ST22_YEAST	P25604 saccharomyc
35	150	20.0	468	2	Q6FS29	Q6fs29 candida gla
36	120.5	16.1	376	2	P78998	P78998 saccharomyc
37	109.5	14.6	445	2	Q75EU1	Q75eu1 ashbya goss
38	109.5	14.6	445	2	AAS50360	Aas50360 ashbya go
39	96.5	12.9	179	2	Q22577	Q22577 caenorhabdi
40	93	12.4	378	2	Q873M7	Q873m7 yarrowia li
41	93	12.4	378	2	Q6C148	Q6c148 yarrowia li
42	89.5	11.9	1867	2	Q9H8B7	Q9h8b7 homo sapien
43	89.5	11.9	4829	1	BIR6_HUMAN	Q9nr09 homo sapien
44	88.5	11.8	694	2	Q759K3	Q759k3 ashbya goss
45	88.5	11.8	694	2	AAS52194	Aas52194 ashbya go

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:24:58 ; Search time 49.1794 Seconds
(without alignments)
809.667 Million cell updates/sec

Title: US-10-053-975A-1_COPY_140_250
Perfect score: 615
Sequence: 1 PVFSRPISASYPPYQATGPP.....ISAVSDKLRWRMKEEMDRAQ 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	615	100.0	307	5	ABP41729	Abp41729 Human ova
2	615	100.0	380	2	AAW19111	Aaw19111 Human tum
3	615	100.0	390	2	AAW93424	Aaw93424 Human NHT
4	615	100.0	390	5	ABP52191	Abp52191 Human tum
5	615	100.0	390	6	AAE34885	Aae34885 Human Tsg
6	615	100.0	390	6	ABG73787	Abg73787 Human tum
7	615	100.0	390	7	ADC35176	Adc35176 Novel hum
8	615	100.0	390	8	ADF91425	Adf91425 TSG101 #S
9	615	100.0	390	8	ADL82957	Adl82957 Human PRO

10	615	100.0	390	8	ADN12256	Adn12256	Human	TSG
11	615	100.0	390	8	ADO43235	Ado43235	Human	TSG
12	615	100.0	390	8	ADO43233	Ado43233	Human	TSG
13	615	100.0	390	8	ADP82614	Adp82614	Human	tum
14	570.5	92.8	381	2	AAW19110	Aaw19110	Mouse	tum
15	570.5	92.8	381	2	AAW93425	Aaw93425	Mouse	tsg
16	570.5	92.8	381	6	ABG73788	Abg73788	Murine	ts
17	570.5	92.8	381	7	ADC35178	Adc35178	Human	tsg
18	570.5	92.8	391	6	AAE34884	Aae34884	Mouse	Tsg
19	570.5	92.8	391	7	ADB85228	Adb85228	Mouse	tum
20	419	68.1	237	4	AAE09328	Aae09328	Human	int
21	209	34.0	331	4	ABB64607	Abb64607	Drosophil	
22	144	23.4	218	4	ABG18833	Abg18833	Novel	hum
23	140.5	22.8	148	3	AAAY86515	Aay86515	Human	gen
24	140.5	22.8	148	5	ABB97431	Abb97431	Novel	hum
25	140.5	22.8	148	6	ABO53679	Abo53679	Novel	hum
26	140.5	22.8	176	4	AAG75132	Aag75132	Human	col
27	138.5	22.5	485	3	AAB57086	Aab57086	Human	pro
28	137.5	22.4	466	2	AAR07084	Aar07084	Recombina	
29	137.5	22.4	466	6	ABO07215	Abo07215	Human	p53
30	137.5	22.4	466	7	ADD47589	Add47589	Human	Pro
31	137.5	22.4	466	7	ADI15879	Adi15879	Human	PP
32	137.5	22.4	466	7	ADJ68571	Adj68571	Human	hea
33	136.5	22.2	258	3	AAB44500	Aab44500	Plant	vir
34	134.5	21.9	244	3	AAG40015	Aag40015	Arabidops	
35	134.5	21.9	245	3	AAG38059	Aag38059	Arabidops	
36	134.5	21.9	245	3	AAG05889	Aag05889	Arabidops	
37	134.5	21.9	247	3	AAG38058	Aag38058	Arabidops	
38	134.5	21.9	247	3	AAG05888	Aag05888	Arabidops	
39	134.5	21.9	263	3	AAG38057	Aag38057	Arabidops	
40	134.5	21.9	274	3	AAG05887	Aag05887	Arabidops	
41	130	21.1	172	4	ABG18832	Abg18832	Novel	hum
42	127.5	20.7	262	8	ADN17284	Adn17284	Chicken	g
43	127.5	20.7	505	2	AAAY07117	Aay07117	Lung	canc
44	127.5	20.7	505	6	ABO07216	Abo07216	Human	p53
45	127.5	20.7	505	7	ADJ68733	Adj68733	Human	hea

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:40:45 ; Search time 10.2168 Seconds
(without alignments)
1045.338 Million cell updates/sec

Title: US-10-053-975A-1_COPY_140_250
Perfect score: 615
Sequence: 1 PVFSRPISASYPPYQATGPP.....ISAVSDKLRWRMKEEMDRAQ 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	186	30.2	404	2	H88650	protein C09G12.9 [
2	145.5	23.7	169	2	T34520	hypothetical prote
3	131.5	21.4	488	1	LUHU7	annexin VII, long
4	127.5	20.7	198	2	D70509	hypothetical prote
5	127.5	20.7	505	2	A53152	annexin XI - human
6	123.5	20.1	503	1	LURB11	annexin XI - rabbi
7	122.5	19.9	279	2	T05421	hypothetical prote
8	122.5	19.9	463	2	S29170	annexin VII - mous
9	121.5	19.8	1880	2	T18531	tractin - medicina
10	119.5	19.4	671	2	T36037	probable export as
11	118	19.2	176	2	A86441	hypothetical prote
12	116.5	18.9	316	2	T20497	hypothetical prote
13	115.5	18.8	177	2	S65780	glycine/proline-ri

14	115.5	18.8	491	2	S14182	DNA-directed RNA p
15	115.5	18.8	650	2	S14181	DNA-directed RNA p
16	115	18.7	240	2	D70894	probable pra prote
17	115	18.7	564	2	H70804	hypothetical prote
18	113	18.4	481	2	F86208	protein F22G5.30 [
19	112	18.2	1357	2	T29265	hypothetical prote
20	112	18.2	1691	1	S22917	collagen alpha 5(I
21	111.5	18.1	1049	1	CGBO7S	collagen alpha 1(I
22	111	18.0	214	2	T10737	extensin-like cell
23	111	18.0	214	2	T09854	proline-rich cell
24	111	18.0	2715	2	T13049	eyelid - fruit fly
25	110.5	18.0	388	2	JC5437	spliceosome-associ
26	110.5	18.0	451	2	B70792	hypothetical prote
27	110.5	18.0	977	2	S14183	DNA-directed RNA p
28	110	17.9	324	2	G86222	hypothetical prote
29	110	17.9	324	2	T51602	shock protein SRC2
30	110	17.9	503	1	LUBO11	annexin XI form A
31	110	17.9	505	1	S23447	annexin XI form B
32	109.5	17.8	1008	2	T04462	hypothetical prote
33	109.5	17.8	1069	2	D85383	hypothetical prote
34	108.5	17.6	428	2	T24769	hypothetical prote
35	108	17.6	467	2	A27677	DNA-directed RNA p
36	108	17.6	1932	1	A28490	DNA-directed RNA p
37	108	17.6	1970	1	S21054	DNA-directed RNA p
38	108	17.6	1970	2	I38186	RNA polymerase II
39	107.5	17.5	179	2	A85217	hypothetical prote
40	107.5	17.5	277	2	T04441	hypothetical prote
41	107.5	17.5	569	2	S42886	collagen - silkwor
42	107.5	17.5	886	2	I50694	collagen alpha 1(I
43	107	17.4	199	2	S14981	extensin class I (
44	107	17.4	299	2	T29956	hypothetical prote
45	106.5	17.3	294	2	A49688	lactose-binding le

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:26:03 ; Search time 53.6817 Seconds
(without alignments)
1189.726 Million cell updates/sec

Title: US-10-053-975A-1_COPY_140_250
Perfect score: 615
Sequence: 1 PVFSRPISASYPPYQATGPP.....ISAVSDKLRWRMKEEMDRAQ 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	615	100.0	390	1 T101_HUMAN	Q99816 homo sapien
2	615	100.0	390	2 Q9BUM5	Q9bum5 homo sapien
3	570.5	92.8	391	1 T101_MOUSE	Q61187 mus musculu
4	552.5	89.8	391	2 Q6IRE4	Q6ire4 rattus norv
5	552.5	89.8	391	2 AAH70951	Aah70951 rattus no
6	545.5	88.7	391	2 Q7TSE5	Q7tse5 rattus norv
7	529	86.0	392	2 Q9I8G8	Q9i8g8 chelonia my
8	405.5	65.9	390	2 Q6IQ70	Q6iq70 brachydanio
9	405.5	65.9	390	2 AAH71540	Aah71540 brachydan
10	383.5	62.4	395	2 Q6P2Z8	Q6p2z8 xenopus tro
11	383.5	62.4	395	2 AAH64236	Aah64236 xenopus t
12	383	62.3	394	2 Q6NUD5	Q6nud5 xenopus lae
13	383	62.3	394	2 AAH68660	Aah68660 xenopus l
14	209	34.0	408	2 Q9VVA7	Q9vva7 drosophila
15	194	31.5	425	2 O76258	O76258 caenorhabdi

16	166.5	27.1	402	2	Q7Q6B6	Q7q6b6 anopheles g
17	152	24.7	249	2	Q8MQZ0	Q8mqz0 drosophila
18	145.5	23.7	148	2	Q9NTQ8	Q9ntq8 homo sapien
19	145	23.6	485	2	Q804G3	Q804g3 brachydanio
20	145	23.6	485	2	AAH68366	Aah68366 brachydan
21	140.5	22.8	148	2	Q6NXQ6	Q6nxq6 homo sapien
22	140.5	22.8	148	2	Q9NZ81	Q9nz81 homo sapien
23	140.5	22.8	148	2	AAH66943	Aah66943 homo sapi
24	137.5	22.4	466	1	ANX7_HUMAN	P20073 homo sapien
25	137.5	22.4	466	2	BAB93492	Bab93492 homo sapi
26	137.5	22.4	466	2	AAP35851	Aap35851 homo sapi
27	137.5	22.4	466	2	CAG28614	Cag28614 homo sapi
28	136	22.1	483	2	Q7T391	Q7t391 brachydanio
29	134.5	21.9	247	2	Q945K9	Q945k9 arabidopsis
30	134.5	21.9	247	2	AAT41866	Aat41866 arabidops
31	130	21.1	664	2	Q6CDQ5	Q6cdq5 yarrowia li
32	129.5	21.1	332	2	Q8QGD9	Q8qgd9 gallus gall
33	128.5	20.9	345	2	Q9ESF4	Q9esf4 mus musculu
34	127.5	20.7	198	2	O86316	O86316 mycobacteri
35	127.5	20.7	201	2	Q7D8K1	Q7d8k1 mycobacteri
36	127.5	20.7	262	2	Q90713	Q90713 gallus gall
37	127.5	20.7	471	2	Q9LD31	Q9ld31 crypthecodi
38	127.5	20.7	505	1	ANXB_HUMAN	P50995 homo sapien
39	127.5	20.7	505	2	CAG29319	Cag29319 homo sapi
40	126.5	20.6	137	2	Q9CQJ5	Q9cqj5 m mus muscu
41	126.5	20.6	171	2	Q7SA74	Q7sa74 neurospora
42	126	20.5	192	2	Q9VKM5	Q9vkm5 drosophila
43	126	20.5	343	2	Q8IVW7	Q8ivw7 homo sapien
44	126	20.5	371	2	Q7Z429	Q7z429 homo sapien
45	126	20.5	868	1	PD6I_HUMAN	Q8wum4 homo sapien

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:24:58 ; Search time 172.793 Seconds
 (without alignments)
 809.667 Million cell updates/sec

Title: US-10-053-975A-1
 Perfect score: 2047
 Sequence: 1 MAVSESQLKKMVSQKYYRDL.....FQLRALMQKARKTAGLSPLY 390

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2047	100.0	390	2 AAW93424	Aaw93424 Human NHT
2	2047	100.0	390	5 ABP52191	Abp52191 Human tum
3	2047	100.0	390	6 ABG73787	Abg73787 Human tum

Untitled									
4	2047	100.0	390	7	ADC35176	Adc35176	Novel	hum	
5	2047	100.0	390	8	AdF91425	Adf91425	TSG101	#S	
6	2047	100.0	390	8	AdL82957	Adl82957	Human	PRO	
7	2047	100.0	390	8	ADN12256	Adn12256	Human	TSG	
8	2047	100.0	390	8	ADO43235	Ado43235	Human	TSG	
9	2047	100.0	390	8	ADO43233	Ado43233	Human	TSG	
10	2047	100.0	390	8	ADP82614	Adp82614	Human	tum	
11	2042	99.8	390	6	AAE34885	Aae34885	Human	Tsg	
12	2002	97.8	380	2	AAW19111	Aaw19111	Human	tum	
13	1945.5	95.0	391	6	AAE34884	Aae34884	Mouse	Tsg	
14	1945.5	95.0	391	7	ADB85228	Adb85228	Mouse	tum	
15	1900.5	92.8	381	2	AAW19110	Aaw19110	Mouse	tum	
16	1900.5	92.8	381	2	AAW93425	Aaw93425	Mouse	tsg	
17	1900.5	92.8	381	6	ABG73788	Abg73788	Murine	ts	
18	1900.5	92.8	381	7	ADC35178	Adc35178	Human	tsg	
19	1404	68.6	307	5	ABP41729	Abp41729	Human	ova	
20	1162	56.8	237	4	AAE09328	Aae09328	Human	int	
21	809.5	39.5	331	4	ABB64607	Abb64607	Drosophil		
22	776	37.9	145	8	ADF91424	Adf91424	TSG101UEV		
23	479	23.4	90	3	AAG01689	Aag01689	Human	sec	
24	455	22.2	398	3	AAG06370	Aag06370	Arabidops		
25	455	22.2	398	8	ADN73283	Adn73283	Thale cre		
26	455	22.2	412	3	AAG06369	Aag06369	Arabidops		
27	435	21.3	379	5	ABP43551	Abp43551	L-lactate		
28	435	21.3	379	8	ADH13697	Adh13697	Human	ENZ	
29	424	20.7	340	3	AAG06371	Aag06371	Arabidops		
30	390	19.1	87	8	ABO55273	Abo55273	Human	gen	
31	380	18.6	322	3	AAG13898	Aag13898	Arabidops		
32	371	18.1	341	4	AAB93473	Aab93473	Human	pro	
33	371	18.1	433	7	ADM29340	Adm29340	Human	nov	
34	346	16.9	146	3	AAB53717	Aab53717	Human	col	
35	339	16.6	452	4	AAU23116	Aau23116	Novel	hum	
36	328	16.0	73	8	ABO55495	Abo55495	Human	gen	
37	267.5	13.1	288	3	AAG13899	Aag13899	Arabidops		
38	161.5	7.9	168	3	AAG13900	Aag13900	Arabidops		
39	161	7.9	485	3	AAB57086	Aab57086	Human	pro	
40	160	7.8	466	6	ABO07215	Abo07215	Human	p53	
41	160	7.8	466	7	ADD47589	Add47589	Human	Pro	
42	160	7.8	466	7	AD115879	Ad115879	Human	PP	
43	160	7.8	466	7	ADJ68571	Adj68571	Human	hea	
44	153	7.5	218	4	ABG18833	Abg18833	Novel	hum	
45	151	7.4	466	2	AAR07084	Aar07084	Recombina		

AAW93424
 ID AAW93424 standard; protein; 390 AA.
 XX
 AC AAW93424;
 XX
 DT 11-JUN-1999 (first entry)

Untitled

Db 61 VPYRGNTYNIPICIWLLDTPYNPPICFVKPTSSMTIKTGKHDVANGKIYLPYLHEWKHP 120

QY 121 QSDLLGLIQVMIVFEGDEPVPFVSRPISASYPYQATGPNTSYMPGMPGISPYPSGYPP 180
 |||||
 Db 121 QSDLLGLIQVMIVFEGDEPVPFVSRPISASYPYQATGPNTSYMPGMPGISPYPSGYPP 180

QY 181 NPSGYPGCPYPGPGYPATTSQYPSQPPVTYVGPSRDGTISEDTIRASLISAVSDKLRW 240
 |||||
 Db 181 NPSGYPGCPYPGPGYPATTSQYPSQPPVTYVGPSRDGTISEDTIRASLISAVSDKLRW 240

QY 241 RMKEEMDRAQAEINALKRTEEDLKKGHQKLEEMVTRLDQEAEDVDKNIELKKDEELSS 300
 |||||
 Db 241 RMKEEMDRAQAEINALKRTEEDLKKGHQKLEEMVTRLDQEAEDVDKNIELKKDEELSS 300

QY 301 ALEKMNQSENNDIDEVIIPTAPLYKQILNLVAEENAIEDTIFYLGALRRCVIDLDVFL 360
 |||||
 Db 301 ALEKMNQSENNDIDEVIIPTAPLYKQILNLVAEENAIEDTIFYLGALRRCVIDLDVFL 360

QY 361 KHVRLSRKQFQLRALMOKARKTAGLSDLX 390
 |||||
 Db 361 KHVRLSRKQFQLRALMOKARKTAGLSDLX 390

RESULT 2

AAE09328
 ID AAE09328 standard; protein; 237 AA.
 XX
 AC AAE09328;
 XX
 DT 19-NOV-2001 (first entry)
 XX
 DE Human intracellular regulatory molecule, tsq101.
 XX
 KW Human; intracellular regulator; cell division; proliferation; therapy;
 KW cancer; infection; wound; developmental abnormality; metabolic problem;
 KW cytostatic; antibacterial; vulnerary; transcription factor; tsq101.
 XX
 OS Homo sapiens.
 XX
 PN US6274312-B1.
 XX
 PD 14-AUG-2001.
 XX
 PF 10-DEC-1997; 97US-00999774.
 XX
 PR 11-DEC-1996; 96US-0032818P.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Gish KC, Seghezzi W, Shanahan F, Lees EM, McClanahan TK;
 XX